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PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCOPHRNCTALGLA
LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPLERSVRERFLPVH

Fig. 1

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GTCCGCCTGAGCCGCTCTCCCTGCTCCAGCAAGGACC
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GCAGAGACAGGGAGCGGCTGGTGTGCCAGTGCACCCCCAGGCACCTTGTGCAGCGG
CCGTGCCGCCAGACAGCCCCACGACGTGAGGCCACTACACGCAG
TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGACCCGCTTCTC
GCCGACGGCTGGTTCTGCTTGAGCACGCATGTGTCACCTGGTGCCTGGCGTGATTGCC
CCGGGCACCCCCAGCCAGAACACGCACTGCGAGCCCCACCGCAACTGCACGCCCTGGGCC
AGCAGCTCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGCCCTGGGCC
CTCAATGTGCCAGGTCTTCTCCATGACACCCGTGCACCAAGCTGCACTGGCTTCCCC
CTCAGCACCGGTACCAAGGAGCTGAGGAGTGTGAGCGTGCCTGTCATGACTTTGTGGCT
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGTCAGGCCCTGAGGCCCCGGAG
GGCTGGGTCCGACACCAAGGGGGCCGCGCGCCTTGCAAGCTGAAGCTGCCTGGCG
CTCACGGAGCTCCTGGGGCGCAGGACGGGGCGCTGCTGGTGCCTGCTGCAGGCGCTG
CGCGTGGCCAGGATGCCGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCCTGTGCAC
TGATCCTGGCCCCCTCTTATTCTACATCCTGGCACCCACTGCACTGAAAGAGG
CTTTTTTTAAATAGAAGAAATGAGGTTNTTAAAAAAAAAAAAAAA

Fig. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCCTGTNGG
GGAGCGTGACCGAGGAGGCACGGGCTTGCACGCCACCAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTCGCGCACGCTGGTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCGGGCACCCCCAGCCA
GAACACGCAGTGCCTAGCCGTGCCCCCAGGCACCTTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGGCTCTCCTCCCATGACACCCCTGTGACCCAGCT
GGCCCTCAATGTGCCAGGCTCTCCTCCCATGACACCCCTGTGACCCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGTACCAAGGAGCTGAGGAGTGTGAG
CGTGCCGTATCGACTTGTGGCTTCCAGGACATCTCCAT

Fig. 3

SEQ ID No:4	178	CA-TTCTGGAACCTACCTGGAGCC
SEQ ID No:5	51	CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAAACGTCCCTCTGNNG
SEQ ID No:6	2	CAGTTCTGGAACTAACCTGGAGGGCTGCCGCTACTGCACGTCCCTCTGNGG
SEQ ID No:3	51	CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAAACGTCCCTCTGNNG
SEQ ID No:5	101	GGAGCNTGAGGGAGGGCANGNGCTGCCACGCCACAAACCGGGCCT
SEQ ID No:6	52	GGAGGGTGAAGGGAGGGCAGGGGCTTGCCACGCCACAAACCGGTGCT
SEQ ID No:7	1	GAGGGCCCCCAGGAGTGGGGGGAGGGT
SEQ ID No:3	101	GGAGCGTGAAGGGAGGGCACGGGTTGCCACGCCACAAACCGGTGCT
SEQ ID No:5	151	GCNGCTGCAGCACGGGNTTCTTCGGCACGCTGNNTTCTGCTTGGAGCAC
SEQ ID No:6	102	GCCCCGTGCCGCCACGGGCTTCTGGGGCACGCTGGTTCTGCTTGGAGCAC
SEQ ID No:7	32	TGGCAGGGGTCAAGGTGCTGGTCCCAGCCTTGACCCCTGAGCTAGGACAC
SEQ ID No:3	151	GCCCCGTGCCACCGGTTCTGGCACGCTGGTCTGCTTGGAGCAC
SEQ ID No:5	201	GCATCGTCCACCTGGTGNCGGGCTGATTGCNCCGGCACCCAGCCA
SEQ ID No:6	152	GCATCGTGTCCACCTGGTGCGGGCTGATTNCCCCGGCACCCAGCCA
SEQ ID No:7	82	CAGTCCCTGACCCCTGTTCTCCCTCTGGCTGCAGGCACCCAGCCA
SEQ ID No:8	1	GCATCGTGTCCACCTGGTGCCGGCTGATTGGGGCACCCAGCCA
SEQ ID No:10	1	CTTGTCCACCTGGTGCCGGTGAATTNCCC-GGGCACCCAGCCA
SEQ ID No:3	201	GCATCGTGTCCACCTGGTGCCGGCTGATTGGGGCACCCAGCCA

Fig. 4.

SEQ ID No: 5	251	GAACACGCA - TGCAAAGCCGTG
SEQ ID No: 7	132	GAACACGGAGN - CC - AGCCCCGTGCCCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No: 8	51	GAACACGGCAG - GCCTAGGCCGTGCCAGGCCACCTTCTCAGCCAGCAGC
SEQ ID No: 10	47	GAACACGGCAGTGCC - AGCCNT - CCCCCCAGGCCACCTTCTCAGCCAGCAGC
SEQ ID No: 9	1	AGCNGTGCNCNNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID No: 3	251	GAACACGGCAGTGCCTAGGCCAGGCCACCTTCTCAGCCAGCAGC
SEQ ID No: 7	182	TCCAGCTCAGAGCAGTGCCAGGCCACCCACCGCAACTGCACGGCCCTGGCCCT
SEQ ID No: 8	101	TCCAGCTCAGAGCAGTGCCAGGCCACCCACCGCAACTGCACGGCCCTGGCCCT
SEQ ID No: 10	97	TCCAGCTCAGAGCAGTGCCAGGCCACCCACCGCAACTGCACGGCCCTGGNC - T
SEQ ID No: 9	36	TCCAGCTCAGAGCAGTGCCAGGCCACCCACCGCAACTGCACGGCCCTGGCCCT
SEQ ID No: 3	301	TCCAGCTCAGAGCAGTGCCAGGCCACCCACCGCAACTGCACGGCCCTGGCCCT
SEQ ID No: 7	232	GGCCCTCAATTGTGCCAGGCCCTTCCCTCATGACACCCCTGTGCACCCAG
SEQ ID No: 8	151	GGCCCTCAATTGTGCCAGGCCCTTCCCTCATGACACCCCTGTGCACCCAGCT
SEQ ID No: 10	147	GGCCCTCAATTGTGCCAGGCCCTTCCCTCATGACACCCCTGTGCACCCAGCT
SEQ ID No: 9	86	GGCCCTCAATTGTGCCAGGCCCTTCCCTCATGACACCCCTGTGCACCCAGCT
SEQ ID No: 3	351	GGCCCTCAATTGTGCCAGGCCCTTCCCTCATGACACCCCTGTGCACCCAGCT
SEQ ID No: 10	197	GCACCTGGCTTCCCCCTCAGCACCCAGGTACCCAGGCTGAGGAGTGTGAG
SEQ ID No: 9	136	GCACCTGGCTTCCCCCTCAGCACCCAGGTACCCAGGCTGAGGAGTGTGAG
SEQ ID No: 3	401	GCACCTGGCTTCCCCCTCAGCACCCAGGTACCCAGGCTGAGGAGTGTGAG
SEQ ID No: 10	247	CGTGGCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
SEQ ID No: 9	186	CGTGGCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
SEQ ID No: 3	451	CGTGGCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT

Fig. 4 (Cont.)

DNA 30942
 HINFR2

M R A L E C P G S I L C L V I A L P A I I P V P A V R G V A I I P I Y P W D O A C I G
 I A P V A V W A A A L A V C E L W A A A M A L P A O V A F T P Y A P E P G S T C A L R C Y Y D O I

DNA 30942
 HINFR2

CRD 1

I S E R L V C A Q C P P C I F V O R P C R A R O S P T T C G P C P P R H Y I O F W H Y L E R C R Y C H V L
 M A O M C C S K C S P C O N A K V F C T K T S D I V C D S C E O S T Y T O I W N W V P E C L S C G S R

DNA 30942
 HINFR2

CRD 2

95 C G E R E E E A R A C H A T H R A C R C A T G F F A H A G . . . F C L E H A S C P P G A G V
 100 C S S O O V E T O A C T R E Q N R I C T C A P G W Y C A L S K O E G C R L C A P L R K C R P G F G V

DNA 30942
 HINFR2

CRD 3

139 I A P G T P S O N T O C O O P C P P G T F S A S S S S S E O C O P H R N C T A L G L A L N V P G S S S
 150 A R P G T E T S D V V C K P C A P G T F S N T T S S T O I C R P H O I C H V V A . . . I P G N A S

DNA 30942
 HINFR2

CRD 4

169 R O T L C T S C T G F P L S T R V P G A E E C R A V I D F V A F Q Q I S I K R L O R L L Q A L E A
 186 R D A V C T S T S . . . P T R S M A P G A V H L P O P V S T R S Q N T O P T P E P S T A P S T S F L L

DNA 30942
 HINFR2

229 P E C G W G P T P . . . R A G R A A L O L K L R R R A L T E L L G A O D G A L L V R L L Q A L R V A R M P
 241 P M G C P S P P A E G S T G D F A L P V G L I V G Y T A U G L L I I G V V N C V I M T Q V K K K P L .

DNA 30942
 HINFR2

287 G L E R S V R E R F L P V H

293 C L Q R E A K V P H L P A D K A R G T Q G P E Q Q H L L I T A P S S S S S L E S S A S A L O R R A

HINFR2

343 P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S P G G H G T O V H V T C I V H V C S S S D

HINFR2

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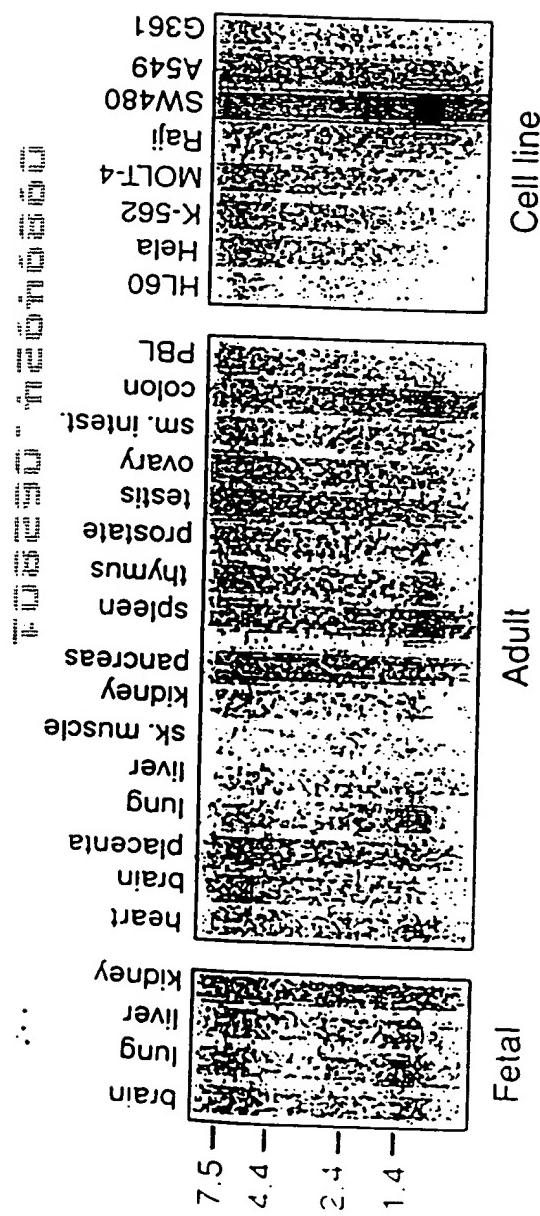
443 S T E E K P L P L G V P D A G M K P S

Fig. 5

DcR3	1	M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A	31
OPG	1	M N K L L C C A L V F L D I S I K W T T Q E T F P - - - - -	25
CRD1			
DcR3	32	E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C	62
OPG	26	- : P K Y L H Y D E E T S H Q L L C D K C P P G T Y L ' K Q H C	54
CRD2			
DcR3	63	R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V	93
OPG	55	T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P	85
CRD3			
DcR3	94	L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G	124
OPG	86	V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E	116
CRD4			
DcR3	125	F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P	155
OPG	117	F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D	147
CRD4			
DcR3	156	G T F S A S S S S S E Q C Q P H R N C T A L G L A L N V P G S	186
OPG	148	G F F S N E T S S S K A P C R K H T N C S V F G L L L T Q K G N	178
CRD5			
DcR3	187	S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D	217
OPG	179	A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R	208
CRD6			
DcR3	218	F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R	247
OPG	209	F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R	239
CRD7			
DcR3	248	A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L	277
OPG	240	I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I	270
CRD8			
DcR3	278	Q A L R V A R M P G L E R S V R E R F L P V H	300
OPG	271	I Q D I D L C E N S V Q R H I G H A N L T F E	293...

Fig. 6

Fig. 7



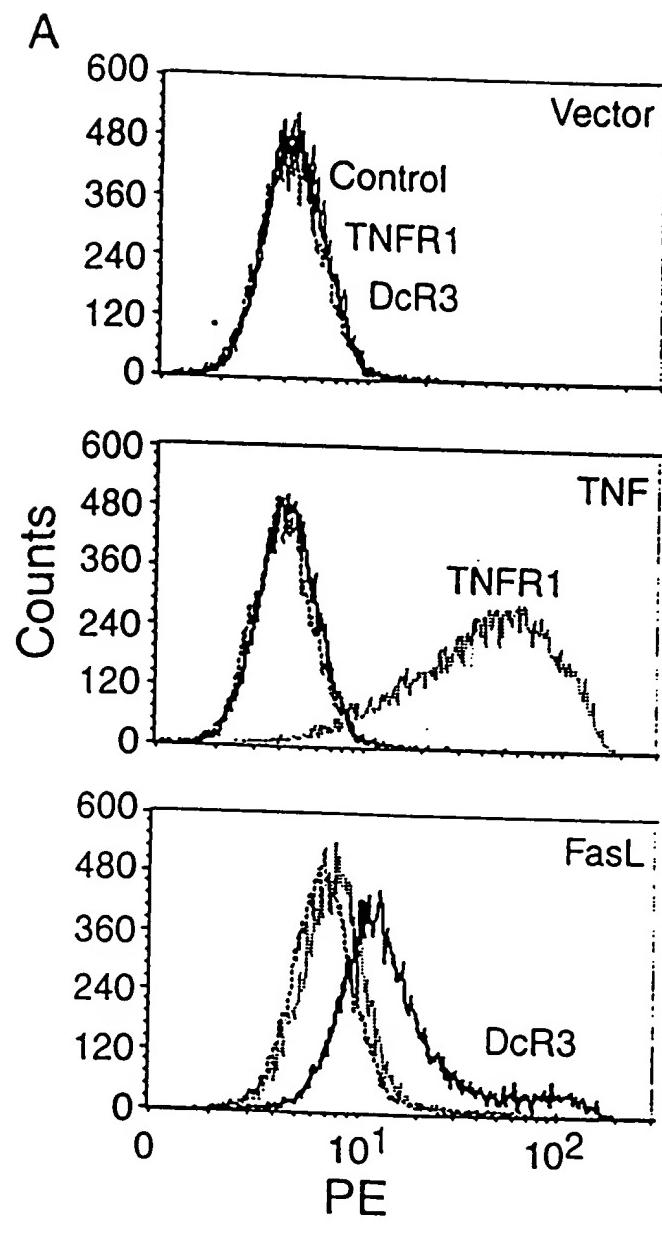
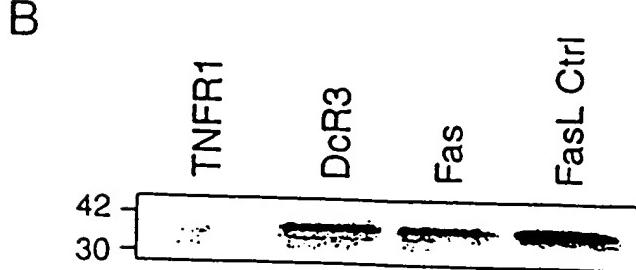


Fig. 8



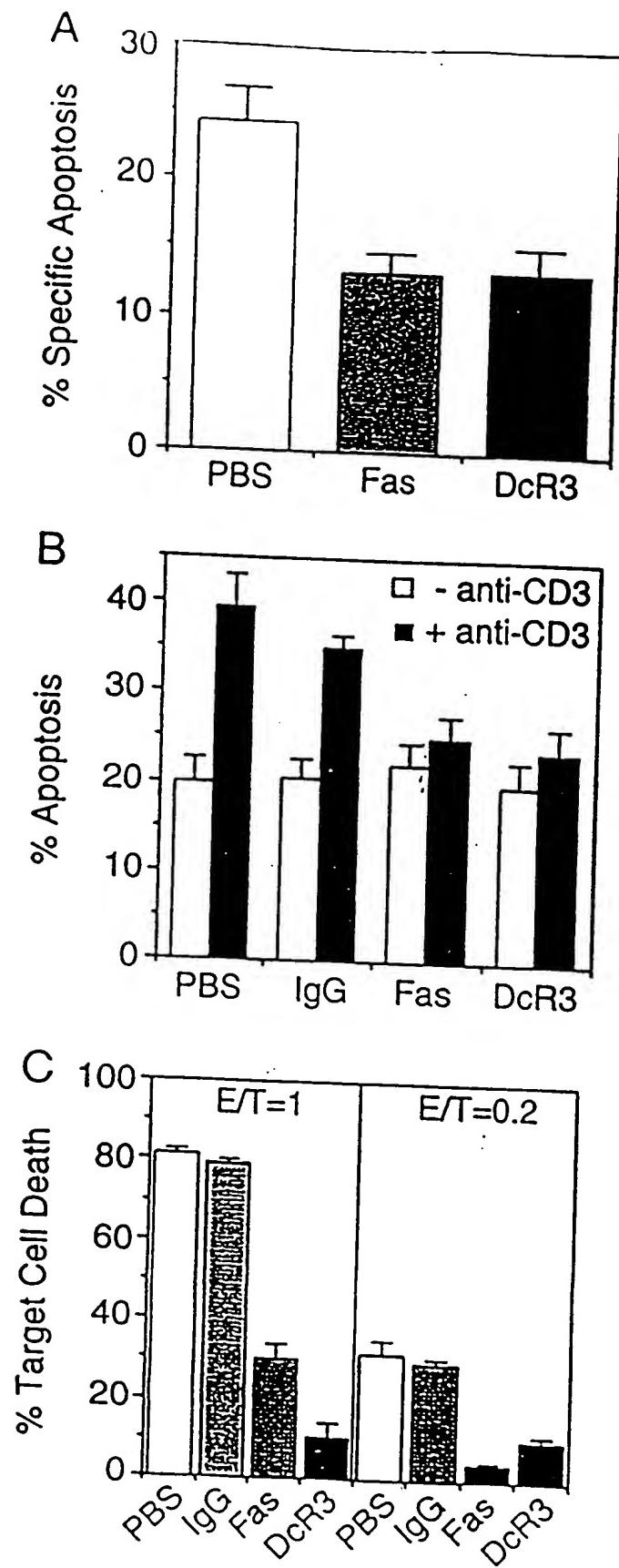


Fig. 9

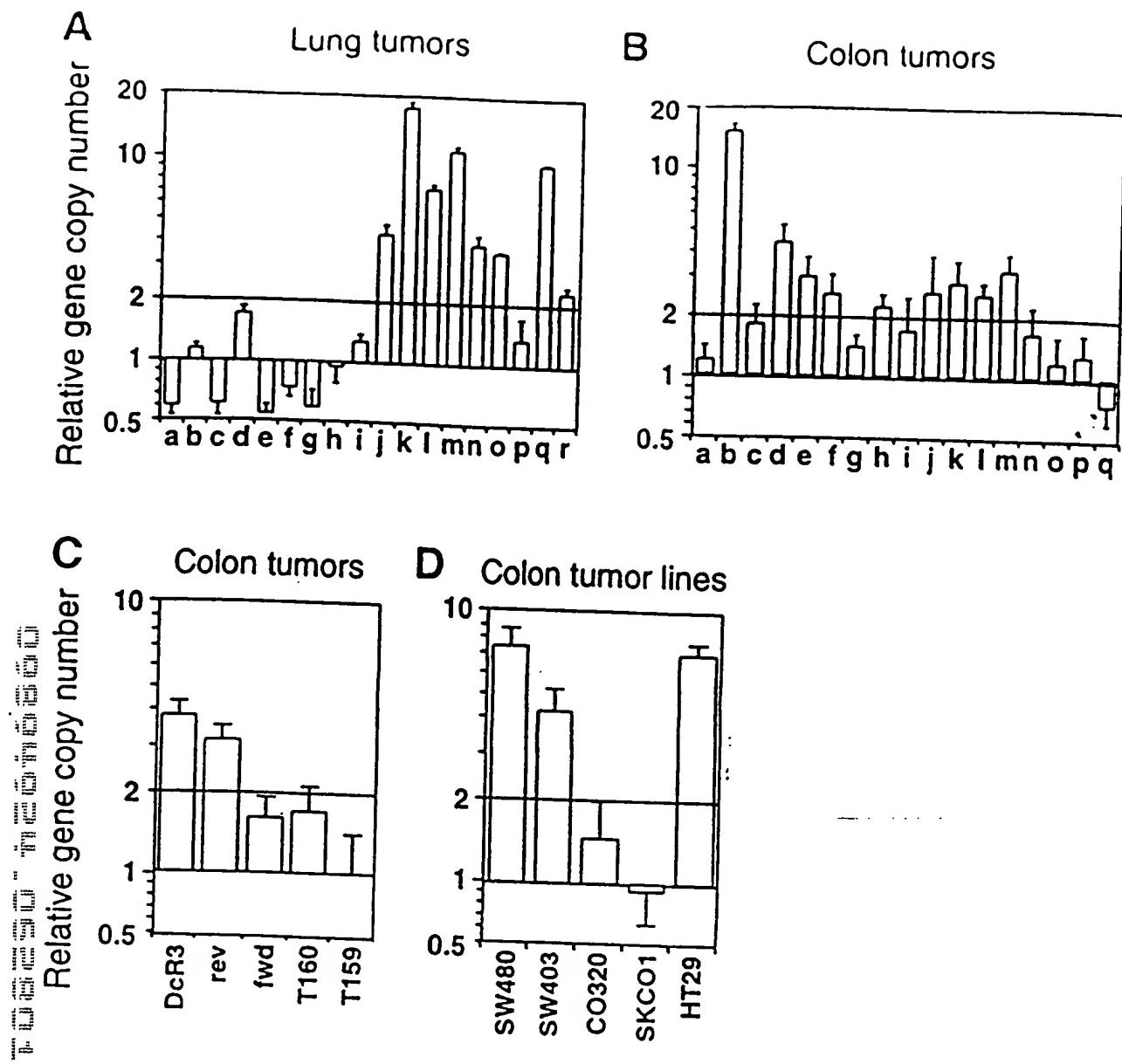


Fig. 10

Fig. 11A

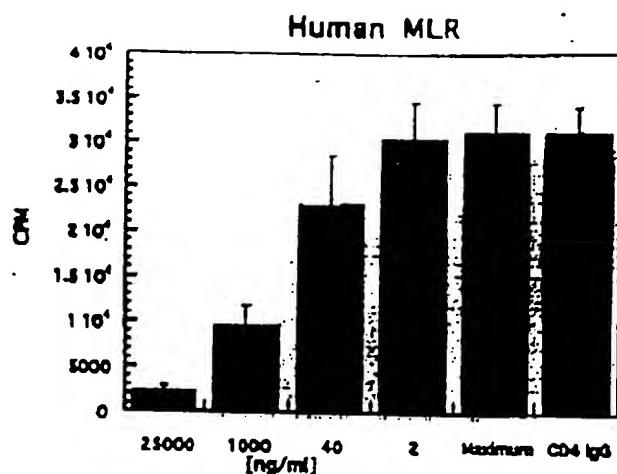


Fig. 11B

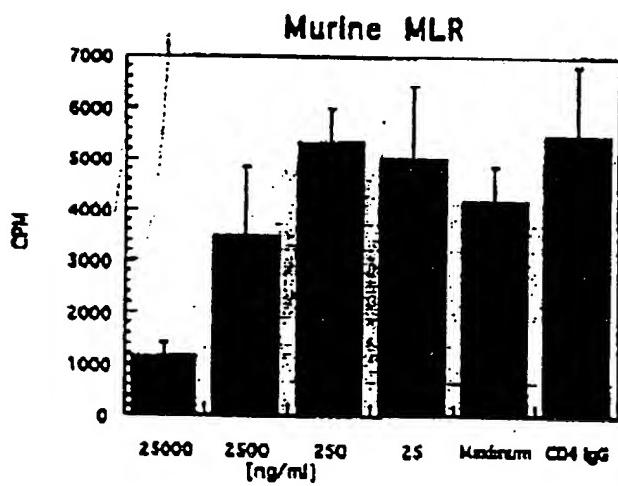


Fig. 11C

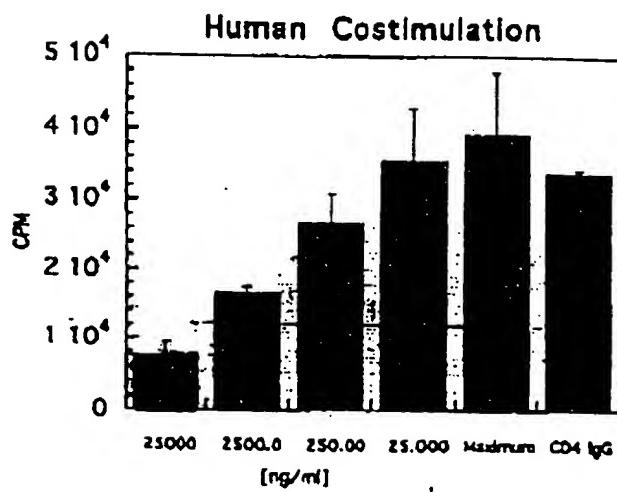


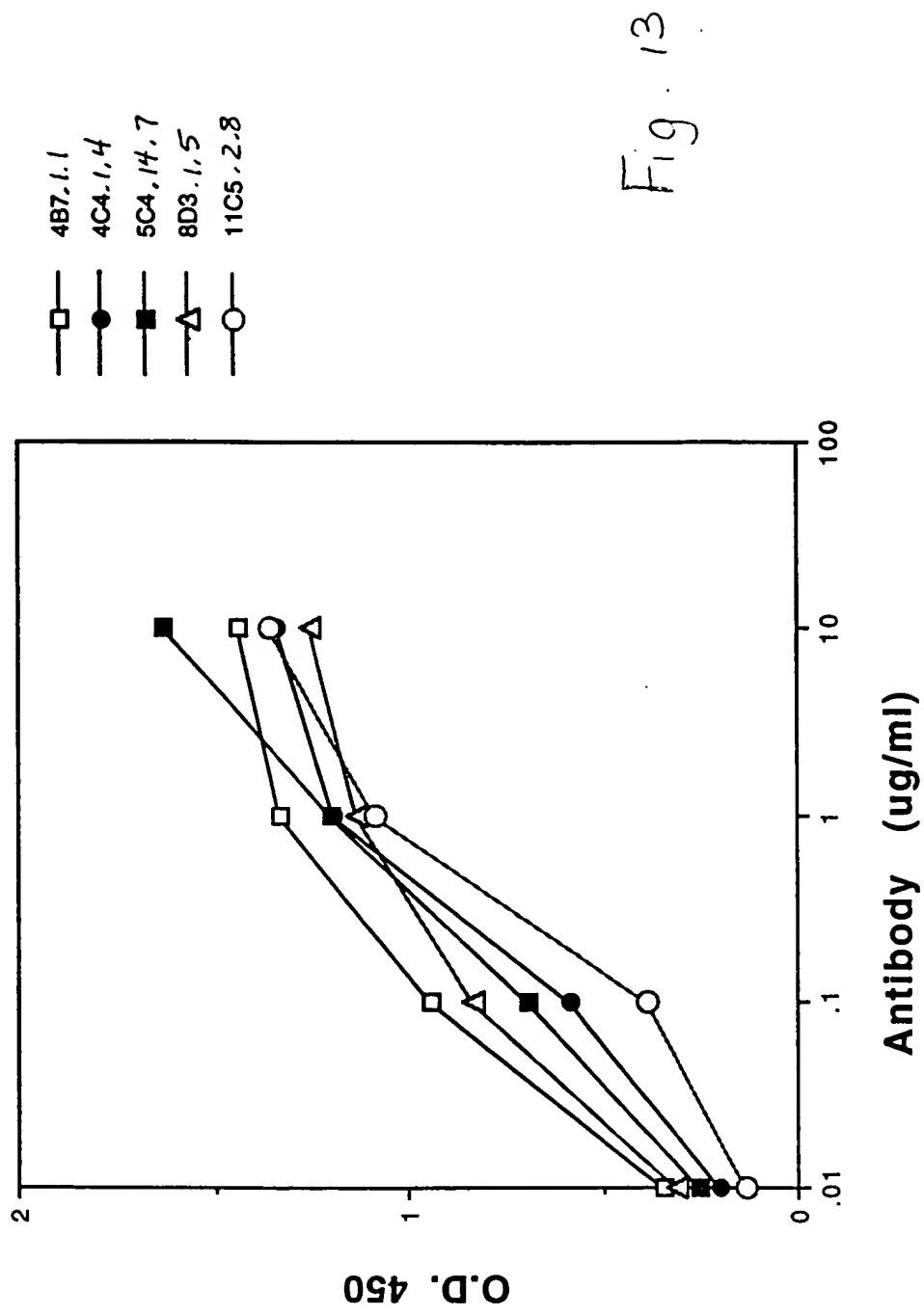
FIGURE 12

mAb	Isotype	Antigen Specificity (ELISA)					t Blocking (ELISA)
		DcR3	DR4	DR5	DcR1	OPG	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

t blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

கால்களை விட விரும்புவதை தெரிய விடுதல்



11. 11. 11. 11. 11. 11. 11. 11. 11. 11. 11. 11. 11.

Fig. 14

